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Sequence Listing could not be accepted.

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Reviewer: Keisha Douglas

Timestamp: [year=2008; month=11; day=20; hr=14; min=22; sec=45; ms=727;]

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Reviewer Comments:

<110> APPLICANT: SmithKline Beecham Biologicals
Ruelle, Jean-Louis

<120> TITLE OF INVENTION: BASB029 Polynucleotides and Polypeptides
from Neisseria Meningitidis

<130> FILE REFERENCE: BM45321

<140> CURRENT APPLICATION NUMBER:09700293

<141> CURRENT FILING DATE:2000-11-13

<150> PRIOR APPLICATION NUMBER: PCT/EP99/03255

<151> PRIOR FILING DATE: 1999-05-07

<150> PRIOR APPLICATION NUMBER: GB 9810276.7

<151> PRIOR FILING DATE: 1998-05-13

<160> NUMBER OF SEQ ID NOS: 6

<170> SOFTWARE: FastSEQ for Windows Version 4.0

<210> SEQ ID NO 1

<211> LENGTH: 1785

<212> TYPE: DNA

<213> ORGANISM: Bacteria

<400> SEQUENCE: 1

Per the above, please do not insert alpha numeric headings in the sequence. The above <213> response for sequence id# 1 is invalid, please insert genus/species response. Please correct the remaining sequences showing similar errors.

Application No: 09700293 Version No: 1.0

Input Set:

Output Set:

Started: 2008-10-27 13:37:45.658
Finished: 2008-10-27 13:37:46.171
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 513 ms
Total Warnings: 6
Total Errors: 0
No. of SeqIDs Defined: 6
Actual SeqID Count: 6

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W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)

<110> APPLICANT: SmithKline Beecham Biologicals
Ruelle, Jean-Louis
<120> TITLE OF INVENTION: BASB029 Polynucleotides and Polypeptides
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<130> FILE REFERENCE: BM45321

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<151> PRIOR FILING DATE: 1998-05-13
<160> NUMBER OF SEQ ID NOS: 6
<170> SOFTWARE: FastSEQ for Windows Version 4.0

<210> SEQ ID NO 1
<211> LENGTH: 1785
<212> TYPE: DNA
<213> ORGANISM: Bacteria
<400> SEQUENCE: 1

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aaagaagtta	cagaagattc	aaattgggga	gtatatattc	acaagaaagg	agtactaaca	300
gccggaacaa	tcacctcaa	agccggcgac	aacctgaaaa	tcaaacaaaa	caccaatgaa	360
aacaccaatg	ccagtagctt	cacctactcg	ctgaaaaaag	acctcacaga	tctgaccagt	420
gttggaactg	aaaaattatc	gtttagcgca	aacagcaata	aagtcaacat	cacaagcgac	480
accaaaggct	tgaatttcgc	gaaaaaaacg	gctgagacca	acggcgacac	cacggttcat	540
ctgaacggta	tcggttcgac	tttgaccgat	acgctgctga	ataccggagc	gaccacaaac	600
gtaaccaacg	acaacgttac	cgatgacgag	aaaaaacgtg	cggcaagcgt	taaagacgta	660
ttaaacgcag	gctggaacat	taaaggcggt	aaacccggta	caacagcttc	cgataacggt	720
gatttcgtcc	gcacttacga	cacagtcgag	ttcttgagcg	cagatacgaa	aacaacgact	780
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tcttctacag	acaaaggcga	aggcttagtg	actgcaaaag	aagtgattga	tgcagtaaac	960
aaggctgggt	ggagaatgaa	aacaacaacc	gctaattggc	aaacagggtc	agctgacaag	1020
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accgtcaaca	ttaatgccgg	caacaacatc	gagattaccc	gcaacggcaa	aaatatcgac	1320
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caacttaaag	gcgtggcgca	aaacttgaac	aaccacatcg	acaatgtgga	cggcaacgcg	1560
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aagagtatga	tggcgatcgg	cggcggcact	tatcgcggcg	aagccgggta	tgccatcggc	1680
tactcaagca	tttccgacgg	cggaaattgg	attatcaaag	gcacggcttc	cggcaattcg	1740
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<211> LENGTH: 594
<212> TYPE: PRT
<213> ORGANISM: Bacteria
<400> SEQUENCE: 2

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Thr	Val	Ala	Thr	Ala	Val	Leu	Ala	Thr	Leu	Leu	Phe	Ala	Thr	Val	Gln		
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Ala	Ser	Thr	Thr	Asp	Asp	Asp	Asp	Leu	Tyr	Leu	Glu	Pro	Val	Gln	Arg		
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Thr	Ala	Val	Val	Leu	Ser	Phe	Arg	Ser	Asp	Lys	Glu	Gly	Thr	Gly	Glu		
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Lys	Glu	Val	Thr	Glu	Asp	Ser	Asn	Trp	Gly	Val	Tyr	Phe	Asp	Lys	Lys		
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Gly	Val	Leu	Thr	Ala	Gly	Thr	Ile	Thr	Leu	Lys	Ala	Gly	Asp	Asn	Leu		
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Lys	Ile	Lys	Gln	Asn	Thr	Asn	Glu	Asn	Thr	Asn	Ala	Ser	Ser	Phe	Thr		
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Tyr	Ser	Leu	Lys	Lys	Asp	Leu	Thr	Asp	Leu	Thr	Ser	Val	Gly	Thr	Glu		
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Lys	Leu	Ser	Phe	Ser	Ala	Asn	Ser	Asn	Lys	Val	Asn	Ile	Thr	Ser	Asp		
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Thr	Lys	Gly	Leu	Asn	Phe	Ala	Lys	Lys	Thr	Ala	Glu	Thr	Asn	Gly	Asp		
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Thr	Thr	Val	His	Leu	Asn	Gly	Ile	Gly	Ser	Thr	Leu	Thr	Asp	Thr	Leu		
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Leu	Asn	Thr	Gly	Ala	Thr	Thr	Asn	Val	Thr	Asn	Asp	Asn	Val	Thr	Asp		
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Asp	Glu	Lys	Lys	Arg	Ala	Ala	Ser	Val	Lys	Asp	Val	Leu	Asn	Ala	Gly		
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			260					265				270					
Glu	Val	Lys	Ile	Gly	Ala	Lys	Thr	Ser	Val	Ile	Lys	Glu	Lys	Asp	Gly		
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Lys	Leu	Val	Thr	Gly	Lys	Asp	Lys	Gly	Glu	Asn	Asp	Ser	Ser	Thr	Asp		
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Lys	Gly	Glu	Gly	Leu	Val	Thr	Ala	Lys	Glu	Val	Ile	Asp	Ala	Val	Asn		
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Lys	Ala	Gly	Trp	Arg	Met	Lys	Thr	Thr	Thr	Ala	Asn	Gly	Gln	Thr	Gly		
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Gln	Ala	Asp	Lys	Phe	Glu	Thr	Val	Thr	Ser	Gly	Thr	Asn	Val	Thr	Phe		
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465 470 475 480
Pro Val Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val
485 490 495
Thr Asn Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn His
500 505 510
Ile Asp Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile
515 520 525
Ala Thr Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met
530 535 540
Ala Ile Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly
545 550 555 560
Tyr Ser Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala
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<210> SEQ ID NO 3

<211> LENGTH: 1776

<212> TYPE: DNA

<213> ORGANISM: Bacteria

<400> SEQUENCE: 3

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acactgttgt ttgcaacggg tcaggcaagt gctaacaatg aagagcaaga agaagattta 180
tatttagacc ccgtacaacg cactgttgcc gtgttgatag tcaattccga taaagaaggc 240
acgggagaaa aagaaaaagt agaagaaaat tcagattggg cagtatatatt caacgagaaa 300
ggagtactaa cagccagaga aatcaccctc aaagccggcg acaacctgaa aatcaaacaa 360
aacggcacaa acttcaccta ctgctgaaa aaagacctca cagatctgac cagtgttggg 420
actgaaaaat tatcgtttag cgcaaacggc aataaagtca acatcacaag cgacaccaaa 480
ggcttgaatt ttgcgaaaga aacggctggg acgaacggcg acaccacggg tcacctgaac 540
ggatttggtt cgactttgac cgatacgctg ctgaataaccg gagcgaccac aaacgtaacc 600
aacgacaacg ttaccgatga cgagaaaaaa cgtgcggcaa gcgttaaaga cgtattaaac 660
gcaggctgga acattaaagg cgttaaaccg ggtacaacag cttccgataa cgttgatttc 720
gtccgcactt acgacacagt cgagttcttg agcgcagata cgaaaacaac gactgttaat 780
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attaaagaaa aagacggtaa gttggttact ggtaaagaca aaggcgagaa tgggttcttct 900
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<210> SEQ ID NO 4

<211> LENGTH: 591

<212> TYPE: PRT

<213> ORGANISM: Bacteria

<400> SEQUENCE: 4

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Thr	Gly	Glu	Lys	Glu	Lys	Val	Glu	Glu	Asn	Ser	Asp	Trp	Ala	Val	Tyr
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Phe	Asn	Glu	Lys	Gly	Val	Leu	Thr	Ala	Arg	Glu	Ile	Thr	Leu	Lys	Ala
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Gly	Asp	Asn	Leu	Lys	Ile	Lys	Gln	Asn	Gly	Thr	Asn	Phe	Thr	Tyr	Ser
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Val	His	Leu	Asn	Gly	Ile	Gly	Ser	Thr	Leu	Thr	Asp	Thr	Leu	Leu	Asn
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	195					200					205				
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225					230				235					240	
Val	Arg	Thr	Tyr	Asp	Thr	Val	Glu	Phe	Leu	Ser	Ala	Asp	Thr	Lys	Thr
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Thr	Thr	Val	Asn	Val	Glu	Ser	Lys	Asp	Asn	Gly	Lys	Lys	Thr	Glu	Val
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Lys	Ile	Gly	Ala	Lys	Thr	Ser	Val	Ile	Lys	Glu	Lys	Asp	Gly	Lys	Leu
	275						280					285			
Val	Thr	Gly	Lys	Asp	Lys	Gly	Glu	Asn	Gly	Ser	Ser	Thr	Asp	Glu	Gly
	290					295				300					
Glu	Gly	Leu	Val	Thr	Ala	Lys	Glu	Val	Ile	Asp	Ala	Val	Asn	Lys	Ala
305					310				315					320	
Gly	Trp	Arg	Met	Lys	Thr	Thr	Thr	Ala	Asn	Gly	Gln	Thr	Gly	Gln	Ala
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Asp	Lys	Phe	Glu	Thr	Val	Thr	Ser	Gly	Thr	Asn	Val	Thr	Phe	Ala	Ser
		340						345					350		
Gly	Lys	Gly	Thr	Thr	Ala	Thr	Val	Ser	Lys	Asp	Asp	Gln	Gly	Asn	Ile
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Ser	Gly	Lys	Val	Ile	Ser	Gly	Asn	Val	Ser	Pro	Ser	Lys	Gly	Lys	Met
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Asp	Glu	Thr	Val	Asn	Ile	Asn	Ala	Gly	Asn	Asn	Ile	Glu	Ile	Thr	Arg
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Asn	Gly	Lys	Asn	Ile	Asp	Ile	Ala	Thr	Ser	Met	Thr	Pro	Gln	Phe	Ser

435 440 445
Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
450 455 460
Gly Asp Ala Leu Asn Val Gly Ser Lys Lys Asp Asn Lys Pro Val Arg
465 470 475 480
Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn Val
485 490 495
Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp Asn
500 505 510
Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr Ala
515 520 525
Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile Gly
530 535 540
Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser Ser
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<210> SEQ ID NO 5
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide
<400> SEQUENCE: 5
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36

<210> SEQ ID NO 6
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Oligonucleotide
<400> SEQUENCE: 6
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34